

## SEQUENCE LISTING

<110> Wong, Justin  
Winter, Jill  
Lalehzadeh, Guita  
Warne, Robert

<120> Compositions and Methods of Therapy for  
Cancers Characterized by Expression of the Tumor-Associated  
Antigen MN/CA IX

<130> PP19155.002/035784/267827

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1380)

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala  
1 5 10 15

48

96

atg cct gtc cat ccc cag agg ttg ccc cg<sup>g</sup> atg cag gag gat tcc ccc  
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro  
35 40 45

144

ttg gga gga ggc tct tct	ggg gaa gat gac cca ctg ggc gag gag gat	
Leu Gly Gly Gly Ser Ser	Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp	
50	55	60

192

ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag  
 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu  
 65 70 75 80

240

gag gat cta cct gga gag gag gat cta cct gga gag gag gag gat cta cct  
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Asp Leu Pro  
85 90 95

288

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gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
          100          105          110

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336

cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat		384	
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn			
115	120	125	
gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg cgc tat gga		432	
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly			
130	135	140	
ggc gac ccg ccc tgg ccc cggtg tcc cca gcc tgc gcg ggc cgc ttc		480	
Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe			
145	150	155	160
cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc		528	
Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala			
165	170	175	
ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ctc cca gaa		576	
Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu			
180	185	190	
ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct		624	
Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro			
195	200	205	
ggg cta gag atg gct ctg ggt ccc ggg cggtg gag tac ccg gct ctg cag		672	
Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln			
210	215	220	
ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act		720	
Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr			
225	230	235	240
gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc		768	
Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser			
245	250	255	
acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg		816	
Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu			
260	265	270	
gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc		864	
Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala			
275	280	285	
tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca		912	
Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser			
290	295	300	
gag act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac		960	
Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp			
305	310	315	320
ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt		1008	
Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys			
325	330	335	

gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser 340 345 350	1056
gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp 355 360 365	1104
tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg 370 375 380	1152
gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala 385 390 395 400	1200
gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu 405 410 415	1248
gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu 420 425 430	1296
gtg cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser 435 440 445	1344
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 <213> Homo sapiens

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 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro  
 35 40 45  
 Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp  
 50 55 60  
 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu  
 65 70 75 80  
 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Asp Leu Pro  
 85 90 95  
 Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp  
 100 105 110  
 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn  
 115 120 125  
 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly  
 130 135 140

Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe  
 145 150 155 160  
 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala  
 165 170 175  
 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu  
 180 185 190  
 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro  
 195 200 205  
 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln  
 210 215 220  
 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr  
 225 230 235 240  
 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser  
 245 250 255  
 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Leu  
 260 265 270  
 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala  
 275 280 285  
 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser  
 290 295 300  
 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp  
 305 310 315 320  
 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys  
 325 330 335  
 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser  
 340 345 350  
 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp  
 355 360 365  
 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg  
 370 375 380  
 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala  
 385 390 395 400  
 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu  
 405 410 415  
 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu  
 420 425 430  
 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser  
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<210> 3  
 <211> 540  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Coding sequence for human CA IX proteoglycan  
 domain construct

<221> CDS  
 <222> (1)...(540)

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 ctt gct cca ggc ctc act gtg caa ctg ctg tca ctg ctg ctt ctg 96  
 Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu  
 20 25 30  
  
 atg cct gtc cat ccc cag agg ttg ccc cggtt gat tcc ccc 144  
 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro  
 35 40 45  
  
 ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat 192  
 Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp  
 50 55 60  
  
 ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag 240  
 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu  
 65 70 75 80  
  
 gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct 288  
 Glu Asp Leu Pro Gly Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro  
 85 90 95  
  
 gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat 336  
 Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp  
 100 105 110  
  
 cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat 384  
 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn  
 115 120 125  
  
 gcc cat agg agc tcg agc atc cta gcc ctg gtt ttt ggc ctc ctt ttt 432  
 Ala His Arg Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe  
 130 135 140  
  
 gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag cac aga 480  
 Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg  
 145 150 155 160  
  
 agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta gcc gag 528  
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 165 170 175  
  
 act gga gcc tag 540  
 Thr Gly Ala \*

<210> 4  
 <211> 179  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for human  
CA IX proteoglycan domain construct

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20 25 30  
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro  
35 40 45  
Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp  
50 55 60  
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu  
65 70 75 80  
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Asp Leu Pro  
85 90 95  
Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp  
100 105 110  
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn  
115 120 125  
Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe  
130 135 140  
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg  
145 150 155 160  
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu  
165 170 175  
Thr Gly Ala

<210> 5

<211> 1089

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for human CA IX carbonic anhydrase  
domain construct

<221> CDS

<222> (1)...(1089)

<400> 5

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1 5 10 15

cct gct cca ggc ctc act gtg caa ctg ctg tca ctg ctg ctt ctg 96  
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu  
20 25 30

atg cct gtc cat ccc ggg gat gac cag agt cat tgg cgc tat gga ggc 144  
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly  
35 40 45

gac ccg ccc tgg ccc cggtg tcc cca gcc tgc gcg ggc cgc ttc cag	192
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln	
50 55 60	
tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg	240
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu	
65 70 75 80	
cgcccccctggaa ctcctggc ttc cag ctc ccgc ccc ctc cca gaa ctg	288
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu	
85 90 95	
cgccctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct ggg	336
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly	
100 105 110	
cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg	384
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu	
115 120 125	
cat ctg cac tgg ggg gct gca ggt cgt ccgc tcg gag cac act gtg	432
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val	
130 135 140	
gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc acc	480
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr	
145 150 155 160	
gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc	528
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala	
165 170 175	
gtg ttg gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat	576
Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr	
180 185 190	
gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag	624
Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu	
195 200 205	
act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac ttc	672
Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe	
210 215 220	
agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt gcc	720
Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala	
225 230 235 240	
cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt gct	768
Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala	
245 250 255	
aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac tct	816
Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser	
260 265 270	

cg <del>g</del> cta cag ctg aac ttc c <del>g</del> a g <del>c</del> g ac <del>g</del> c <del>g</del> c <del>c</del> t tt <del>g</del> aat g <del>g</del> g c <del>g</del> a gt <del>g</del>	864		
Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val			
275	280	285	
att gag gcc tcc ttc cct gct g <del>g</del> a g <del>t</del> g gac agc agt c <del>c</del> t c <del>g</del> g g <del>c</del> t g <del>c</del> t	912		
Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala			
290	295	300	
gag cca gtc cag ctg aat tcc tgc ctg gct g <del>g</del> t gac atc c <del>t</del> a g <del>g</del> cc	960		
Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala			
305	310	315	320
ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc g <del>c</del> g ttc ctt g <del>t</del> g	1008		
Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val			
325	330	335	
cag atg aga agg cag cac aga agg gga acc aaa ggg g <del>g</del> t g <del>t</del> g agc tac	1056		
Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr			
340	345	350	
cg <del>c</del> cca gca gag gta g <del>c</del> c g <del>a</del> g act g <del>g</del> a g <del>c</del> c tag	1089		
Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *			
355	360		

<210> 6  
 <211> 362  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Polypeptide encoded by coding sequence for human  
 CA IX carbonic anhydrase domain construct

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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu			
20	25	30	
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly			
35	40	45	
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln			
50	55	60	
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu			
65	70	75	80
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu			
85	90	95	
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly			
100	105	110	
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu			
115	120	125	
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val			
130	135	140	
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr			
145	150	155	160
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala			
165	170	175	

Val	Leu	Ala	Ala	Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr
180						185								190	
Glu	Gln	Leu	Leu	Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Gly	Ser	Glu	
195						200								205	
Thr	Gln	Val	Pro	Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe
210						215								220	
Ser	Arg	Tyr	Phe	Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala
225						230								240	
Gln	Gly	Val	Ile	Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala
245						250								255	
Lys	Gln	Leu	His	Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser
260						265								270	
Arg	Leu	Gln	Leu	Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val
275						280								285	
Ile	Glu	Ala	Ser	Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala
290						295								300	
Glu	Pro	Val	Gln	Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala
305						310								320	
Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	Val
325						330								335	
Gln	Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr
340						345								350	
Arg	Pro	Ala	Glu	Val	Ala	Glu	Thr	Gly	Ala						
355						360									

<210>	7															
<211>	978															
<212>	DNA															
<213>	Artificial Sequence															
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<223>	Coding sequence for glu-tagged human CA IX															
carbonic anhydrase domain construct																
<221>	CDS															
<222>	(1) ... (978)															
<400> 7																
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Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala	
1															15	
cct	gct	cca	ggc	ctc	act	gtg	caa	ctg	ctg	tca	ctg	ctg	ctt	ctg		96
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Leu	Ser	Leu	Leu	Leu		
20															30	
atg	cct	gtc	cat	ccc	cag	agg	ttg	ccc	cg	atg	cag	gag	gct	agc	gaa	144
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Ala	Ser	Glu	
35															45	
tac	atg	cca	atg	gaa	caa	gaa	ccc	cag	aat	aat	gcc	cac	agg	gac	aaa	192
Tyr	Met	Pro	Met	Glu	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys	
50															60	

gaa	ggg	gat	gac	cag	agt	cat	tgg	cgc	tat	gga	ggc	gac	ccg	ccc	tgg	240	
Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	Gly	Asp	Pro	Pro	Trp		
65							70			75					80		
ccc	cg	gtg	tcc	cca	gcc	tgc	g	gc	cg	tcc	ccg	gtg	gat	288			
Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp		
							85			90				95			
atc	cg	cc	cag	ctc	gcc	tcc	tgc	ccg	gcc	ctg	cgc	cc	ctg	gaa	336		
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu		
							100			105				110			
ctc	ctg	gg	tcc	cag	ctc	ccg	cc	cca	gaa	ctg	cgc	ctg	cgc	aac	384		
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn		
							115			120				125			
aat	gg	cac	agt	gtg	caa	ctg	acc	ctg	cct	gg	cta	gag	atg	gct	432		
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala		
							130			135				140			
ctg	gg	cc	gg	cg	gag	ta	cg	gg	ct	ctg	ca	ct	ctg	cac	tgg	480	
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp		
							145			150				155			
gg	g	ct	g	gt	cc	gg	tc	g	ag	ca	ac	gt	gaa	gg	cac	cgt	528
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg		
							165			170				175			
ttc	cct	gg	gag	atc	ca	gt	gt	ca	ct	ag	ac	gg	ttt	gg	aga	576	
Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg		
							180			185				190			
gtt	gac	gag	gg	tt	gg	cg	cc	gg	g	gg	ct	gg	gg	tt	gg	624	
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala		
							195			200				205			
ttt	ctg	gag	gg	cc	g	aa	aa	ac	gt	ta	g	ct	ca	cc	ac	672	
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Leu	His	Thr		
							210			215				220			
ctc	tct	gac	acc	ct	tg	gg	gg	cct	gg	gac	tct	cg	ct	ca	ac	720	
Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn		
							225			230				235			
ttc	cga	g	cg	cag	cct	tt	aa	at	gg	cg	gt	at	gag	gg	tc	tt	768
Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe		
							245			250				255			
cct	g	gt	g	ac	ag	gt	c	cg	g	ct	g	ca	gt	c	ct	816	
Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	Leu		
							260			265				270			
aat	tcc	tgc	ctg	g	ct	g	ct	gg	at	ct	gg	tt	ttt	gg	ct	864	
Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu		
							275			280				285			

ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag	912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln	
290 295 300	
cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta	960
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val	
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gcc gag act gga gcc tag	978
Ala Glu Thr Gly Ala *	
325	
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<223> Polypeptide encoded by coding sequence for	
glu-tagged human CA IX carbonic anhydrase domain	
construct	
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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu	
20                   25                   30	
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu	
35                   40                   45	
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys	
50                   55                   60	
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp	
65                   70                   75                   80	
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp	
85                   90                   95	
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu	
100                  105                  110	
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn	
115                  120                  125	
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	
130                  135                  140	
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp	
145                  150                  155                  160	
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	
165                  170                  175	
Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg	
180                  185                  190	
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	
195                  200                  205	
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr	
210                  215                  220	
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn	
225                  230                  235                  240	
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe	
245                  250                  255	

Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	Leu
260							265						270		
Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu
275							280						285		
Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	Val	Gln	Met	Arg	Arg	Gln
290							295					300			
His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr	Arg	Pro	Ala	Glu	Val
305							310			315			320		
Ala	Glu	Thr	Gly	Ala											
							325								

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<223>	Coding sequence for glu-tagged mutant human CA IX															
carbonic anhydrase domain construct																
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atg	gct	ccc	ctg	tgc	ccc	agc	ccc	tgg	ctc	cct	ctg	ttg	atc	ccg	gcc	48
Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala	
1				5						10				15		
cct	gct	cca	ggc	ctc	act	gtg	caa	ctg	ctg	ctg	tca	ctg	ctg	ctt	ctg	96
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Leu	
20				25							30					
atg	cct	gtc	cat	ccc	cag	agg	ttg	ccc	cg	atg	cag	gag	gct	agc	gaa	144
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Ala	Ser	Glu	
35							40				45					
tac	atg	cca	atg	gaa	caa	gaa	ccc	cag	aat	aat	gcc	cac	agg	gac	aaa	192
Tyr	Met	Pro	Met	Glu	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys	
50				55						60						
gaa	ggg	gat	gac	cag	agt	cat	tgg	cgc	tat	gga	ggc	gac	ccg	ccc	tgg	240
Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	Gly	Asp	Pro	Pro	Trp	
65				70					75			80				
ccc	cgg	gtg	tcc	cca	gcc	tgc	gcf	ggc	cgc	tcc	cag	tcc	ccg	gtg	gat	288
Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp	
85							90					95				
atc	cgc	ccc	cag	ctc	gcc	ttc	tgc	ccg	gcc	ctg	cgc	ccc	ctg	gaa		336
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu	
100							105				110					
ctc	ctg	ggc	tcc	cag	ctc	ccg	ccg	ctc	cca	gaa	ctg	cgc	ctg	cgc	aac	384
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn	
115							120				125					

aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct	432
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	
130 135 140	
ctg ggt ccc ggg cg <sup>g</sup> gag tac cg <sup>g</sup> gct ctg cag ctg caa ctg cag tgg	480
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu Gln Leu Gln Trp	
145 150 155 160	
ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt	528
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	
165 170 175	
ttc cct gcc gag atc caa gtg gtt cac ctc agc acc gcc ttt gcc aga	576
Phe Pro Ala Glu Ile Gln Val Val His Leu Ser Thr Ala Phe Ala Arg	
180 185 190	
gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc	624
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	
195 200 205	
ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag ctc cac acc	672
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr	
210 215 220	
ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg aac	720
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn	
225 230 235 240	
ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc ttc	768
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe	
245 250 255	
cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag ctg	816
Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu	
260 265 270	
aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc ctc	864
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu	
275 280 285	
ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag	912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln	
290 295 300	
cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta	960
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val	
305 310 315 320	
gcc gag act gga gcc tag	978
Ala Glu Thr Gly Ala *	
325	

<210> 10  
<211> 325  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for  
glu-tagged mutant human CA IX carbonic anhydrase  
domain construct

<400> 10

Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala  
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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu  
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Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu  
35 40 45  
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys  
50 55 60  
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp  
65 70 75 80  
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp  
85 90 95  
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu  
100 105 110  
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn  
115 120 125  
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala  
130 135 140  
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu Gln Leu Gln Trp  
145 150 155 160  
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg  
165 170 175  
Phe Pro Ala Glu Ile Gln Val Val His Leu Ser Thr Ala Phe Ala Arg  
180 185 190  
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala  
195 200 205  
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr  
210 215 220  
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn  
225 230 235 240  
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe  
245 250 255  
Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu  
260 265 270  
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu  
275 280 285  
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln  
290 295 300  
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val  
305 310 315 320  
Ala Glu Thr Gly Ala  
325